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Incorporating Uncertainty in Population Assessments

Incorporation de l'incertitude dans l'évaluation des populations

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ABSTRACT

The best approach to minimize the risk of management or conservation failure is to incorporate uncertainty in assessments and use that to guide low risk management and conservation decisions. There is a wide array of methods for incorporating uncertainty and it is not always clear to the analyst which method should be used for a particular assessment. This paper looks at various methods that are used or could be used to incorporating uncertainty in assessments of marine mammal populations. It attempts to order those methods according to similarity and to give a short description of each of them. It presents examples of uncertainty methods used on marine mammal assessments and relevant methods used in other disciplines concerned with risk assessment. Pros and cons of each method are discussed. The paper concludes by addressing the question of whether there should be a limited set of methods used for DFO marine mammal stock assessments or whether methods should be chosen according to the circumstances. It concludes that the appropriateness of the various methods for incorporating uncertainty varies depending on the type of uncertainty and the information available.

RÉSUMÉ

La meilleure démarche pour réduire au minimum le risque d'échec de gestion ou de conservation est d'intégrer l'incertitude dans les évaluations et d'en tenir compte pour prendre des décisions prudentes en matière de gestion et de conservation. Il existe une vaste gamme de méthodes d'intégration de l'incertitude, et il n'est pas toujours évident pour un analyste de déterminer laquelle convient le mieux à une évaluation donnée. Dans ce document, nous présentons diverses méthodes qui sont utilisées ou qui pourraient l'être pour intégrer l'incertitude dans les évaluations de populations de mammifères marins. Nous avons regroupé ces méthodes en fonction de leur similarité et nous décrivons chacune brièvement. Nous présentons également des exemples d'application de certaines de ces méthodes ainsi que d'autres méthodes pertinentes utilisées dans d'autres domaines où l'évaluation des risques est nécessaire. Nous discutons des avantages et des inconvénients de chacune des méthodes présentées. Nous abordons la question à savoir si le MPO devrait limiter le nombre de méthodes qu'il utilise pour évaluer les populations de mammifères marins ou si le choix des méthodes devrait dépendre des circonstances propres à chaque situation. Nous concluons que la pertinence des diverses méthodes d'intégration de l'incertitude varie en fonction du type d'incertitude et de l'information disponible.

INTRODUCTION

Assessments are conducted with some model of the process being assessed. In some cases, several models that represent competing hypothesis of the processes at play may be assessed and their relative merits in "explaining" these processes may be compared. An example of a population model is:

$$N_{t+1} = N_t e^{r\Delta t} - h_{t+1} \qquad [1]$$

Here, the parameters are "r", the population's rate of increase, and "h", the harvest on the population. "N_0", the population size at time "0" can also be a model parameter if used at the start of a population projection. Model parameters and the incorporation of their uncertainty in assessments are the topic of this paper.

Why incorporate uncertainty in population assessments? Historically, management of marine resources have been based on "best estimates" of a population's response to harvesting (Wade 1998, 2001a). The objective was to maintain a sustainable harvest or to harvest at the maximum sustainable yield. In recent decades, with the collapse of many fisheries and marine mammal hunts, it has been increasingly recognised that such an approach is flawed. It does not make allowance for random events (stochasticity), errors of model parametization (bias or statistical uncertainty) or inadequate model choice (ignorance of important parameters). As a result, a managed population may behave quite differently from what models based on best estimates predict (Hilborn and Walters 1992; Rice et al. 1999; Richards and Schnute 2000; Rice and Rivard 2001). In fact, deviations from best estimates are more likely than the alternative.

The best approach to minimize the risk of management or conservation failure is to incorporate uncertainty in assessments and use that to guide low risk management and conservation decisions (Wade 2001a, Ferson 2002). There is a wide array of methods for incorporating uncertainty and it is not always clear to the analyst which method should be used for a particular assessment. This paper looks at various methods that are used or could be used to incorporating uncertainty in assessments of marine mammal populations. I attempt to order those methods according to similarity and to give a short description of each of them. I present examples of uncertainty methods used on marine mammal assessments and relevant methods used in other disciplines concerned with risk assessment. Pros and cons of each method are discussed. The paper concludes by addressing the question of whether there should be a limited set of methods used for DFO marine mammal stock assessments or whether methods should be chosen according to the circumstances.

Types of uncertainty

There are several sources of uncertainty in population assessments. There is uncertainty in the choice of the model and their parameters that influence the process in question, e.g. growth of a population. The uncertainty of parameters can be simple ignorance of the values to use for a parameter, bias and statistical uncertainty in its estimation, and stochastic or deterministic variation between years. Methods for dealing with these problems vary according to the source of uncertainty and the information available.

Data-poor and data-rich situations

More often than not, population status, growth rate and life history parameters of marine mammal populations are poorly specified because of a lack or a paucity of data to estimate them. Some parameters such as survivorship-at-age or finite rate of increase are practically impossible to estimate for most marine mammal populations. In such cases, biologists have resorted to using plausible ranges for the parameters based on analogies with populations or species which have a similar life history and for which there is enough data (e.g. Doidge, D.W. 1990; Reilly and Barlow

1986; Kingsley 1989; Wade and Angliss 1997; Wade 1998; Bourdages et al. 2002; Richard et al. 2003). In a few data-rich cases, there are long-term studies with datasets on hunt statistics, survey indices or individual-based life history parameters (Brault and Caswell.1993; Olesiuk et al. 1990; Wells and Scott 1990; Raftery et al. 1995). Even in those cases, there may be biases that are difficult to assess.

Methods of incorporating uncertainty

I will distinguish two types of uncertainty methods: methods that delimit conservative point limits and methods that generate an uncertainty distribution for the quantity of interest. The point limit methods are often used in data-poor cases while the distribution methods require more data and therefore are used in data-rich cases. There are exceptions in both cases, as we will see below. For example, some point limit methods (e.g. PBR) are distributional methods in disguise because they use information or make an assumption on the distribution of at least one parameter. On the other hand, some distribution methods are new approaches to uncertainty characterization and propagation that have been developed for cases where information about the uncertainty distribution is "not-so-rich". For each method, I give examples or cite studies where the method is described more fully . The examples given are loosely based on the case of the E. Hudson Bay beluga population (Bourdages et al. 2000).

A. Point limit methods

Under Point limit methods, I grouped those uncertainty methods that use known or assumed limits on the uncertainty distribution of model parameters used to estimate a quantity of interest. They are presented from the simplest, Worst-case scenarios, to the most complex, Robust point limit methods.

A.1 Worst-Case Scenarios

Because of the uncertainty and difficulty in characterising phenomena in natural systems, risk analysts have sometimes resorted to simply use extreme values of parameters (Ferson 2002). This approach is conservative and does not require the definition of distributional properties of parameters, nor does it require any knowledge of the dependence between parameters of the model. Worst-case scenarios involve simple arithmetic as would be done for deterministic "best estimate" calculations.

Let's consider the following example: we know the number of individual beluga seen in the last aerial survey (Aug. 2001) of Eastern Hudson Bay (229) to be the only belugas known to be alive at the time for that region. If this number combined with the most conservative maximum rate of increase (0.02) for a cetacean (Bourdages et al 2001) was used to calculate the yield of the population in absence of a hunt, the result would be only 4 animals per year. That would be much less than the estimated catch on the stock (Bourdages et al. 2001).

Worst-case scenarios are criticised for being potentially hyper-conservative (Ferson 2002). They are also narrowly focused by ignoring any available information on distributional properties of model parameters

A.2 Interval Methods

Interval methods are an extension of the above, a sort of worst case-best case scenario. A range [min, max] of possible values for each parameter is defined. These methods are useful if distributional properties of the parameters are difficult to measure. It is also useful whether the source of uncertainty is bias or statistical error.

The calculations involved in interval arithmetic are an extension of point estimate calculations. They involve two points [min, max] by two points [min, max] calculations. The rules are simple but some operations such as subtraction and division require care. There is software for doing interval calculations (among other uncertainty calculi methods), e.g. RAMAS Risk Calc 4.0 (Ferson 2002) and Vladik Kreinovich's website http://www.cs.utep.edu/interval-comp/intsoft.html.

Continuing with the Eastern Hudson Bay beluga example, let's say we know that the population could not be more than 10,000 animals which is the historical maximum estimated for that population and that it is likely that it has declined by at least half its size in the last two century. The population size interval would then range between 229 and 5,000 with a range of yields between 4 and 200 if the rate of increase is an interval 0.02-0.04. Those results give a simple idea of the extent of uncertainty in the assessment Eastern Hudson Bay population size but they say nothing on the most likely values or the shape of the distribution. Note that we could also generate an interval using conservative assumptions about the survey estimates probability distribution, such as using the 1% and 99% percentiles. A normal distribution could be used for the right tail and a more skewed distribution (e.g. lognormal) for the left tail (note: see Halley and Inchausti 2002 for a discussion of lognormalilty in animal populations). Simpler assumptions based on analogies and deductive reasoning, therefore more subjective, have been made for intervals of parameters such as rate of increase limit (e.g.: see Table 2 in Bourdages et al. 2001).

The use of intervals to define parameters in assessment makes for simple arithmetic but interval analysis is criticised for being potentially over-conservative if based on extreme outliers or biased measurements (Ferson 2002).

A.3 Robust Point Limit Methods

Robust point limit methods are methods which have the appearance of being point methods but are in fact based on distributional methods which have undergone robustness trials (using Monte Carlo methods – see below) to ensure that biases in the input data will have a low probability of causing a departure from stated management or conservation goals. They are therefore distributional methods in disguise. The best known robust point limit method is the PBR or potential biological removal used by the National Marine Fisheries Service for marine mammal populations (Wade 1998).

It is a point limit method in the sense that it uses point values rather than distributions but it is based on choices of a distribution of population size and a production model that are conservative enough to be robust to biases. The potential biological removal is calculated as follows (Wade 1998):

$$PBR = N_{MIN} \frac{1}{2} R_{MAX} F_R$$

where N_{MIN} is the minimum population estimate was calculated as the lower limit of the two-tailed 60% confidence interval of the log-normal distributed best abundance estimate, *i.e.* equivalent to the 20th percentile of the log-normal distribution, i.e.:

$$N_{MIN} = \frac{\hat{N}}{\exp\left(z\sqrt{\ln(1+CV(N)^2}\right)}$$

R_{MAX} is the maximum rate of increase estimated for the species (note: for cetacean species where it is not known, it is assumed to be 0.04, and for pinnipeds 0.12). It is scaled by ½ to allow for the possibility of density dependent effects, which may act to reduce the population's intrinsic rate of increase. The conservative assumption is that the rate of increase follows a simple logistic response to population size and therefore the rate of increase is only at a maximum when the population is very small and is halved when the population is half of carrying capacity level.

F_R is a recovery factor applied to discount the PBR to increase the probability of population growth if it is considered depleted or endangered. It varies between 0.1 for endangered stocks, 0.50 for stocks of unknown status or listed as depleted or threatened; Fr = 1.0 for stocks thought to be at Optimum Sustainable Population level as defined by the US National Marine Fisheries Service (i.e.: above MSYL).

Most of the calculations are simple arithmetic, which makes this method appealing. The only slight difficulty is in the calculation of Nmin, which requires the evaluation of the normal variate z and a logarithm. That can easily be done in an Excel spreadsheet using its mathematical and statistical functions. Bourdages et al (2001), calculated the PBR for the Eastern Hudson Bay beluga population to range between 3 and 17 depending on the population estimate used, rate of increase and recovery factor used. Interestingly, the result of using the most conservative assumption for Fr (0.1) is similar to our worst-case scenario example above.

The PBR is a relatively simple method, which by the nature of its conservative assumptions will almost inevitably, barring catastrophic events, lead to the growth of a population of marine mammals if it is depleted or to maintaining a large population if the population is large. In those ways, the PBR serves goals defined in NMFS policy for managing human-induced mortality on marine mammals. One problem with the PBR is that it is narrowly focused on population recovery to "optimal population size". However, growth of populations or maintaining a large population are not the only goals that managers might be interested in evaluating. In addition, like worst-case and interval analyses, the black-box PBR approach hides a lot of details on distributional information of parameters and the rationale behind the assumptions made about parameters (e.g. R_{max} = 0.04 for cetaceans) when there is ignorance about their true value. In circumstances where decision-making is consensual, such as for co-management organisations, it is a better policy to be explicit about all knowledge and assumptions used in models. Assurance that all participants in decision-making are informed of all factors and assumptions affecting an assessment is more likely to promote trust in that assessment and ultimately decisions that are more acceptable to all parties (Pinkerton 1989, Richard and Pike 1993).

In summary, point limit methods are quick-and-dirty ways to gauge problems and they have some benefit when information about the uncertainty distribution of parameters is not available. If information about the distributional properties are available, it is preferable to use uncertainty distribution methods. They will make the assessment more credible and informative to decision-makers.

B. Uncertainty distribution methods

The following methods require some means of characterizing the uncertainty of model parameters in order to propagate it to the model outputs (e.g. future population size or yield). They range from traditional statistical methods to a suite of newer approaches for characterising and propagating uncertainty.

B.1 Empirical statistical and resampling methods

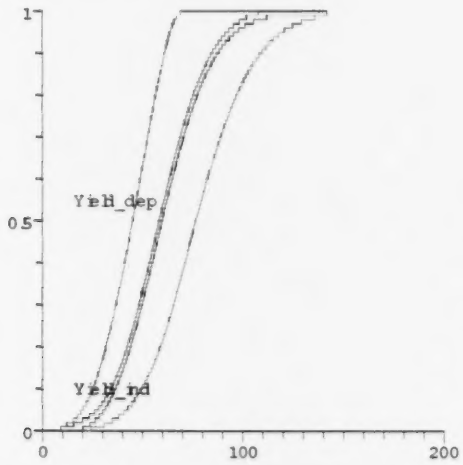
When two or more parameters of a model have statistical uncertainty that can be estimated, the calculation of the distribution of the model results is achieved by propagating the probability distributions of the different parameters using probability calculations, known as convolutions. For all but the simplest cases, such as linear combinations of normal distributions, the convolution of two distributions is either impossible analytically or requires elaborate methods of numerical integrations (Morgan and Henrion 1990). With the access to fast personal computers and software, the more common approach today is to use numerical resampling methods (bootstrap and Monte Carlo methods).

Resampling methods either use a parametric distribution model (e.g. normal, lognormal, triangular ... etc.) to generate samples (parametric bootstrap) or simply resample the data available for a

quantity of interest (empirical bootstrap). This is achieved in the first case by randomly selecting a value of the uncertain quantity from its parametric probability distribution (parametric bootstrap) and in the second case from the data itself (empirical bootstrap), where each data point has an equal probability of being picked. Sampling is carried out hundreds or thousands of times (*ergo* "resampling"). Several algorithms make resampling calculations more efficient and faster. The most common ones are Random or Median Latin Hypercube methods.

Uncertainty propagation in model calculations using uncertain parameters is achieved by Monte Carlo methods. This is simply conducted by operations between individual samples from a bootstrap of each of the model parameters. This process is repeated hundreds or even thousands of times. There are many software engines to apply Monte Carlo methods. Some of the more accessible ones are RAMAS Library of Software (www.ramas.com), Analytica (www.lumina.com), @Risk (www.palisade.com), and Crystal Ball (www.decisioneering.com). There are also resampling functions or modules in many programming languages and high-end statistical software packages, such as R (www.r-project.org), S-PLUS (www.insightful.com) and AD Model Builder (http://otter-rsch.com/admodel.htm).

Analysts using Monte Carlo methods often assume that the uncertain quantities are statistically independent. If uncertain model parameters are not independent, uncertainty propagation becomes much more difficult (Ferson 1994, 1995). That is why dependence between parameters is often ignored. Off-the-shelf resampling software are not suited for convolutions of dependent parameters. In addition, the dependence between uncertain quantities is rarely known. Monte Carlo results obtained under the assumption of independence may over- or underestimate the true distribution tails of the quantity of interest. Using the Eastern Hudson Bay as an example, assuming that the population size 'N' has a normal distribution Norm(mean, stdev) defined by *Norm(2000,600)* and expert advice suggests that annual variation in the rate of increase 'r' can be characterised by a triangular distribution Triang(min, mode, max) defined by *Triang(0.02,0.03,0.04)*. Using Risk Calc 4.0, the distribution of uncertainty of the range of yields after one year was calculated as the product of 'N' and 'r' for the case where they are independent and the case where the assumption of independence cannot be justified.



Note: the tails theoretically go to zero and positive infinity, but of course, they get very small.

In the case where independence cannot be assumed (Yield_dep), the results are a range of possible cumulative distributions whose tails are substantially different from the CDF of yield of the independent case (Yield_ind). It is reasonable to assume that a population's rate of growth and the population's size are not independent for big populations where density dependent effects are likely to take place and for very small populations where survival or reproduction may be lowered, so

called "Allee effects" (Dennis 2002). Risk Calc 4.0 uses a method based on Fréchet's inequality (Ferson 2002; Ferson and Long 1994; Ferson and Burgman 1995) to determine the bounds of possible probability distributions if one cannot assume independence between the parameters being convolved.

When there exists a long-term data series for a population (e.g. population size estimates over several years or individual survivorships over decades), one can attempt to estimate parameters such as the rate of increase or the population size at carrying capacity in logistic or modified logistic models. Optimization methods using goodness-of-fit or maximum likelihood can be used to find the parameters that yield the best model "fit". Alternative models can also be compared to determine the model that has the "best of the best fits", but also the least complexity and the most realism for ease of biological interpretation (Hilborn and Mangel 1997; Haddon 2001).
Estimation of parameters and comparisons of models are computationally intensive and therefore are most often conducted using computer algorithms for optimization and resampling. An example is given by Bourdages et al. (2002) where the rate of increase of the Eastern Hudson Bay beluga population was estimated from "best fits" of different models to series of population size and catch estimates, using Risk Optimizer (www.palisade.com). Risk Optimizer uses a so-called 'genetic' algorithm to iteratively try different combination of values of model parameters, calculate a loss function (in this case minimizing the mean sum of squares of model fit to the survey data) and continue until new trials show relatively little improvements to the fit.

Bourdages et al. (2001) compared different models for their fit to the data and commented on the plausibility of the optimised parameters. They did not use any formal method of selecting between models. They used some of the best-fit estimates of "r" to project the population size into the future and show what different scenarios of catch would result. To do so, they use @Risk (www.palisade.com) to run a Monte Carlo in which the uncertainty distribution of the 2001 population was modelled using a normal assumption, e.g.: Norm(mean, stddev), to model the uncertainty of the start population. On the other hand, they used point estimates for "r" estimate because Risk Optimizer does not produce an uncertainty distribution for "optimal" set of parameter results. The lack of uncertainty distribution for "r" probably resulted in an underestimate of the uncertainty distribution of the Monte Carlo results. It might be possible to obtain a goodness of fit profile from the trial parameters stored by Risk Optimizer during the iterative process and use the calculated MSS for each trial to build an uncertainty distribution for "r" and "N_i". However, the software does not reject duplicate trials (Marco 2000) so it could be very tedious to eliminate them manually when there are several thousands trials. An additional filtering algorithm would be required to do so.
Likelihood methods are also used to estimate parameters using an iterative optimization algorithm (Hilborn and Mangel 1997, Wade 2001a). Such algorithms are available in high end statistical software, such as those are listed above. Risk Optimizer and Optiquest (www.decisioneering.com) are off-the shelf optimizing software that could also be used for that purpose with the caveats mentioned above. Likelihood ratio tests and similar methods can be used to select models when likelihood profiles are used to fit the models. The Akaike information criterion is one method that is increasingly used for model selection (Hilborn and Mangel 1997, Wade 2001a).

Likelihood methods are powerful ways to generate uncertainty distributions of model estimates and to compare competing models. However, these methods require that the analysts decide which parametric distribution (e.g. normal, lognormal, etc) can best characterise the probability distribution of the uncertain quantity being estimated. The likelihood profile is based on a comparison between the predictions of that parametric model with the model estimate for each trial's set of parameters. In some cases, the choice of a particular distribution can be justified by probabilistic arguments or by examination of the data (Hilborn and Mangel 1977) but, in many cases, the probability model is not obvious and the data is too scarce to know with what shape the uncertain quantities probability distribution should be modelled.

B.2 Bayesian statistical methods

Bayesian methods use Bayes theorem to estimate a posterior probability from both a prior distribution and the likelihood distribution for the quantity of interest. The prior distribution characterises prior belief, e.g. a plausible range of values that the quantity may take. The likelihood is the probability of getting the data assuming a certain parametric distribution for the quantity. The posterior is the Bayesian model result, i.e.: the probability distribution of values for the estimated quantity given the data. Bayesians argue that this method is the only way to estimate an uncertain quantity, i.e.: the probability of a value for the quantity of interest. They argue that empirical (traditional) statistical methods can only estimate the probability of the sample data given a statistical model explaining the process (Ellison 1996; Wade 2002).

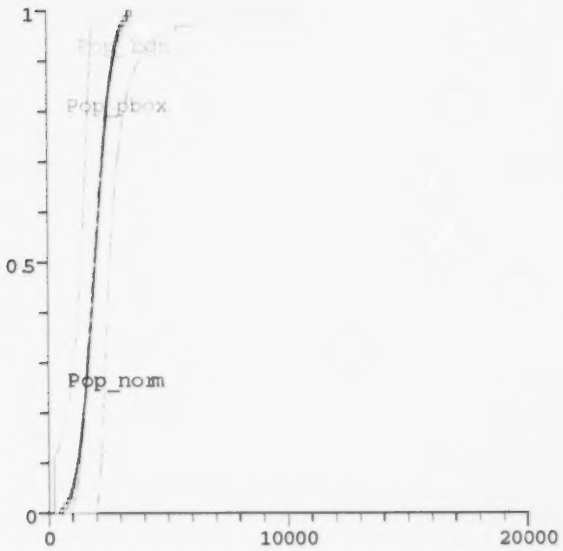
Bayesian methods have become popular with some ecologists (Dixon and Ellison 1996; Hilborn and Mangel 1997) and marine mammal population biologists (Wade 2001a, 2002). They are being used for whale population assessments (e.g. Raftery and Zeh 1998, Wade 2001b, Innes and Stewart 2002). Nevertheless, these methods remain controversial for many scientists. Bayesian statistics is a significantly different way of doing science and it has been suggested that claims made by Bayesian scientists have yet to be substantiated (Dennis 1996).

Bayesian methods require complex calculation also best done by optimization and resampling algorithms. The most popular algorithm for Bayesian estimation is Monte Carlo Markov Chain, MCMC (Gelman, et al. 1997). There are functions and modules in high-end statistical software such as as R (www.r-project.org), S-PLUS (www.insightful.com) and AD Model Builder (http://otter-rsch.com/admodel.htm). For novice programmers, the most accessible one is probably BUGS, Bayesian inference Using Gibbs Sampling, (http://www.mrc-bsu.cam.ac.uk/bugs/). To my knowledge, there is no commercial implementation of Bayesian estimation methods. The learning curve is rather steep because of the complexity of the methods and the lack of user-friendly software renders their implementation very difficult for novice analysts.

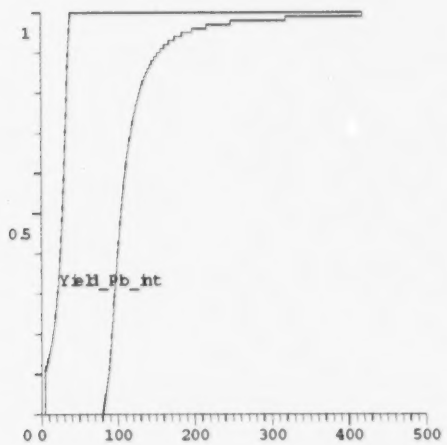
B.3 Probability Bounds

We may know that a parameter has statistical uncertainty but its probability distribution may not be known. Therefore, there are a number of distributions that could have the parameters that have been estimated from the data. In such cases, an analyst will often be forced to assume a particular probability distribution. That may be fine if one is mainly concerned with the estimate but if the quantities of interest are at the tails of the distribution, the choice of a particular distribution can cause an under-estimation of those quantities.

For example, we may know that the population estimate is 2000 and its standard deviation is 600. We may then assume that the population is normally-distributed as defined by N(2000, 600) or that it is lognormally distributed, i.e.: LogN(2000,600). The figure below shows the normal cumulative probability distribution (in blue) and the lognormal (in green), which in this case are almost identical, except for a slight departure at the tails. Around them are probability bounds of all the possible CDFs that could be defined if one knows only the mean and standard deviation and makes no assumption on the shape of the distribution. Probability bounds are also called "p- boxes" for short. Following the case of the eastern Hudson Bay beluga survey, we have constrained the left bound of the p-box (as well as the normal and lognormal) at 229 since that is the number known with certainty to exist because they were counted during the survey.



Probability bounds or "p-boxes" also provide a quality-assurance check on the independence assumption. Their calculation is complex and requires computer algorithms. RAMAS Risk Calc 4.0 (www.ramas.com) is to my knowledge the only software that does those kinds of calculations. In the example above, the constrained p-box was defined by the Risk Calc function minmeanstddev(229,2000,600). RiskCalc also allows mathematical operations between p-boxes or between p-boxes and intervals or fuzzy numbers. For example, using the above lognormal p-box for population size and an assumed interval of [0.02,0.04] for the uncertainty in the rate of increase, we obtain a Yield p-box as shown in the figure below. We can also get an uncertainty interval for a percentile from the p-box by using the Risk Calc Cut function, e.g. cut(Yield_pb_int,0.025) = [4.8, 82.2].

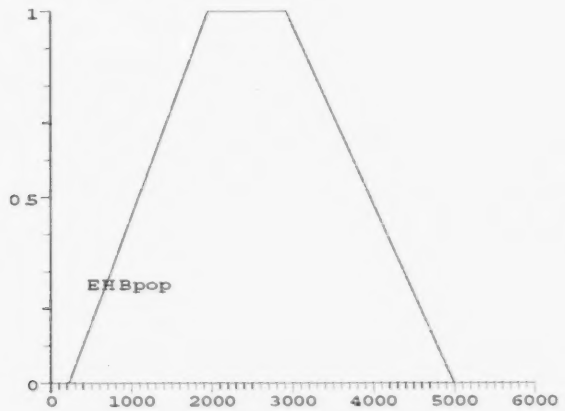


The advantage of being able to conduct quality assurance on distributional assumptions using p-boxes is immediately obvious. Risk Calc also provides functions to tighten the bounds if more

information becomes available about the distribution's shape (Ferson 2002). One problem with p-boxes are that they must truncate infinite tails. Also, repeated p-box parameters in calculations can generate p-boxes that are not optimal, i.e.: are overly conservative (Ferson 2002).

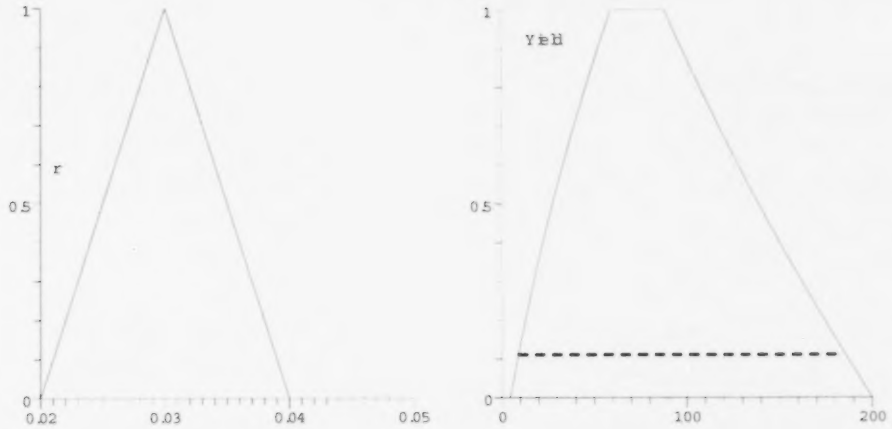
B.4 Fuzzy Numbers and Possibility Theory

Fuzzy numbers and possibility theory are new methods and theory first developed by Zadeh (1965, 1978) to quantify non-statistical forms of uncertainty. Non-statistical uncertainty refers to our ignorance about the value or distribution of a quantity. It includes measurement error and imprecision of various kinds (Ferson 2002).



A fuzzy number can be thought of as a stack of intervals that narrows vertically toward the most "possible" values of an uncertain quantity. For example, let's assume we know that the eastern Hudson Bay beluga population is at least the number of animals seen during a survey (229) and at most 5,000 or half the supposed historical abundance prior to commercial whaling. On inspection of dive data, we also think that the population is most likely to be the estimated 1155 corrected for 40% and 60% diving animals (1/0.6 to 1/0.4) plus the number (39) seen in the estuary (1964-2927), we get a trapezoid-shaped fuzzy number that can be defined as follows [229, 1964, 2927, 5000]. The y axis in the figure above represents the possibility level for any particular value of that population size.

Now let us assume that we know the lowest value of the population annual rate of increase is 0.02, the most likely is 0.03 and the highest it could be is 0.04 then we have a triangular fuzzy number for r defined by [0.02, 0.03, 0.04]. The yield calculation becomes simply the product of the two fuzzy numbers, which is similar to the product of the stack of intervals that form the two fuzzy numbers. The figures below show graphic representations of the fuzzy numbers for 'r" and for the yield obtained from the product of population size and rate of increase fuzzy numbers.



Fuzzy arithmetic is relatively simple since it is an extension of interval analysis but it can be tedious if the shapes of the polygons are complex. There is software to simplify fuzzy calculations. Risk Calc 4.0 (www.ramas.com) is user-friendly software that has many tools for fuzzy arithmetic, as well as other uncertainty methods discussed in this paper. It also provides several functions for fuzzy calculus, such as the calculation of limits based on a particular possibility level. For example, the broken line set at possibility level 0.1 in the Yield figure above defines the interval [9, 187]. That interval was obtained by the Risk Calc fuzzy function "cut(Yield, 0.1)".

An interval defined by a possibility level in a fuzzy number is similar to a confidence interval defined by an alpha level for a statistical probability distribution, except that it defines uncertainty of any kind, not simply statistical uncertainty. Unlike statistical methods or even Bayesian methods that rely on probabilistic arguments and are therefore limited to propagation of statistical uncertainty, fuzzy numbers allows the characterization of any kind of uncertainty, including bias and ignorance. Bias is a systematic form of uncertainty and is not propagated correctly by statistical methods (Wilson 1952). Fuzzy arithmetic does not use assumptions about dependence between quantities used for statistical uncertainty calculi, nor could it make use of such assumptions or evidence about these dependencies (Ferson 2002).

The problem with fuzzy numbers and their theoretical underpinning, possibility theory, is that they are still controversial in science. They constitute a new approach to uncertainty propagation that is based on weaker mathematical axioms than statistical theory and, unlike statistical methods, it has not had a long history and expert guidance is not well developed. It is often considered overly conservative, being intermediate in conservativeness between interval analysis and Monte Carlo methods (Ferson 2002).

Conclusions

In my introduction to the paper, I stated the question of whether there should be a limited set of methods used for DFO marine mammal stock assessments or whether uncertainty methods should be chosen according to the circumstances. With the examples above, I have tried to show that there is more than one way to incorporate uncertainties in assessments of marine mammals and that their appropriateness varies depending on the type of uncertainty and the information available. Some are appropriate for statistical uncertainty (empirical and Bayesian statistical methods), others for ignorance and bias (fuzzy numbers) and some for both (worst-case scenarios, intervals, probability bounds). The data-poor cases force the analyst to use conservative and

sometimes subjective methods (worst-case scenarios, intervals, fuzzy numbers, probability bounds) while data-rich cases afford greater use of statistical methods (empirical and Bayesian statistical methods, estimation by optimization methods) but bias may still force the use of hybrid methods such as probability bounds and intervals or fuzzy numbers. Debate about the appropriateness of Bayesian versus empirical methods is still raging among statisticians, let alone biologists. It could be a while before there is consensus on the conditions under which one should use either approach.

In this paper, I tried to reduce the complexity of these numerous competing methods and to simplify the arguments about their usefulness but the incorporation of uncertainty in assessments remains a complex field of investigation. Despite the complexities, an analyst should not be paralyzed. The most important thing is to move away from "best estimates" assessments which are now known to be too risky and to make an effort to incorporate uncertainty as best as possible within their means. Any investment in time and effort to that end will aid decision-makers to choose management and conservation options that have a lower risk of detrimental effects on the populations of interest (Wade 2001a).

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